

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/808,124B

Source: TFW16

Date Processed by STIC: 12-20-04

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IFW16

RAW SEQUENCE LISTING

DATE: 12/20/2004

PATENT APPLICATION: US/09/808,124B

TIME: 13:08:44

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12202004\I808124B.raw

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5 <110> APPLICANT: Potter, Robert
6     Rosenthal, Kim
9 <120> TITLE OF INVENTION: High Fidelity Reverse Transcriptases and Uses Thereof
12 <130> FILE REFERENCE: 0942.5030001/RWE
15 <140> CURRENT APPLICATION NUMBER: 09/808,124B
17 <141> CURRENT FILING DATE: 2001-03-15
20 <150> PRIOR APPLICATION NUMBER: 60/189,454
22 <151> PRIOR FILING DATE: 2000-03-15
25 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: PatentIn version 3.0
32 <210> SEQ ID NO: 1
34 <211> LENGTH: 47
36 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
44 <223> OTHER INFORMATION: Synthetic oligonucleotide template
48 <400> SEQUENCE: 1
49 gagttacagt gtttttggtc cagtctgtag cagtgtgtga atggaag          47
52 <210> SEQ ID NO: 2
54 <211> LENGTH: 18
56 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
64 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
68 <400> SEQUENCE: 2
69 cttccattca cacactgc          18
72 <210> SEQ ID NO: 3
74 <211> LENGTH: 21
76 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
84 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
88 <400> SEQUENCE: 3
89 gaagatcgca ctccagccag c          21
92 <210> SEQ ID NO: 4
94 <211> LENGTH: 298
96 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
104 <223> OTHER INFORMATION: lacZa peptide in M13mp19 from SuperScript II RT and
105     SuperScript II H203R T306K F309N
109 <400> SEQUENCE: 4
110 agcgcaacgc aattaatgtg agttagctca ctcataggc accccaggct ttacacttta    60

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112 tgcttcgaggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120
114 gctatgacca tgattacgcc aagcttgcac gcctgcaggt cgactctaga ggatccccgg 180
116 gtaccgagct cgaattcact ggccgtcggt ttacaacgtc gtgactggga aaaccctggc 240
118 gttacccaac ttaatcgct tgcagcacat ccccttttcg ccagctggcg taatagcg 298
122 <210> SEQ ID NO: 5
124 <211> LENGTH: 1575
126 <212> TYPE: DNA
128 <213> ORGANISM: Moloney-Murine Leukemia Virus
131 <220> FEATURE:
133 <221> NAME/KEY: CDS
135 <222> LOCATION: (1)..(1575)
138 <400> SEQUENCE: 5
139 atg acc cta aat ata gaa gat gag cat cgg cta cat gag acc tca aaa 48
140 Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys
141 1 5 10 15
143 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag 96
144 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
145 20 25 30
147 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 144
148 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
149 35 40 45
151 ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 192
152 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
153 50 55 60
155 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 240
156 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
157 65 70 75 80
159 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac 288
160 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
161 85 90 95
163 acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct 336
164 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
165 100 105 110
167 gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc 384
168 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
169 115 120 125
171 acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc aag cgg gtg gaa 432
172 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu
173 130 135 140
175 gac atc cac ccc acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc 480
176 Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu
177 145 150 155 160
179 cca ccg tcc cac cag tgg tac act gtg ctt gat tta aag gat gcc ttt 528
180 Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe
181 165 170 175
183 ttc tgc ctg aga ctc cac ccc acc agt cag cct ctc ttc gcc ttt gag 576
184 Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu
185 180 185 190
187 tgg aga gat cca gag atg gga atc tca gga caa ttg acc tgg acc aga 624

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188	Trp	Arg	Asp	Pro	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	
189			195				200					205					
191	ctc	cca	cag	ggt	ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	672
192	Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	
193		210					215					220					
195	cac	aga	gac	cta	gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	720
196	His	Arg	Asp	Leu	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	
197	225					230					235					240	
199	cta	cag	tac	gtg	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	768
200	Leu	Gln	Tyr	Val	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	
201					245					250					255		
203	tgc	caa	caa	ggt	act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	816
204	Cys	Gln	Gln	Gly	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly	
205				260					265					270			
207	tat	cgg	gcc	tcg	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	864
208	Tyr	Arg	Ala	Ser	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	
209			275				280					285					
211	tat	ctg	ggg	tat	ctt	cta	aaa	gag	ggt	cag	aga	tgg	ctg	act	gag	gcc	912
212	Tyr	Leu	Gly	Tyr	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	
213		290				295					300						
215	aga	aaa	gag	act	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	960
216	Arg	Lys	Glu	Thr	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	
217	305					310					315					320	
219	cta	agg	gag	ttc	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	1008
220	Leu	Arg	Glu	Phe	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	
221				325						330					335		
223	ggg	ttt	gca	gaa	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	1056
224	Gly	Phe	Ala	Glu	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	
225			340						345					350			
227	act	ctg	ttt	aat	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	1104
228	Thr	Leu	Phe	Asn	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	
229			355				360					365					
231	aag	caa	gct	ctt	cta	act	gcc	cca	gcc	ctg	ggg	ttg	cca	gat	ttg	act	1152
232	Lys	Gln	Ala	Leu	Leu	Thr	Ala	Pro	Ala	Leu	Gly	Leu	Pro	Asp	Leu	Thr	
233		370				375					380						
235	aag	ccc	ttt	gaa	ctc	ttt	gtc	gac	gag	aag	cag	ggc	tac	gcc	aaa	ggt	1200
236	Lys	Pro	Phe	Glu	Leu	Phe	Val	Asp	Glu	Lys	Gln	Gly	Tyr	Ala	Lys	Gly	
237	385					390					395					400	
239	gtc	cta	acg	caa	aaa	ctg	gga	cct	tgg	cgt	cgg	ccg	gtg	gcc	tac	ctg	1248
240	Val	Leu	Thr	Gln	Lys	Leu	Gly	Pro	Trp	Arg	Arg	Pro	Val	Ala	Tyr	Leu	
241				405						410					415		
243	tcc	aaa	aag	cta	gac	cca	gta	gca	gct	ggg	tgg	ccc	cct	tgc	cta	cgg	1296
244	Ser	Lys	Lys	Leu	Asp	Pro	Val	Ala	Ala	Gly	Trp	Pro	Pro	Cys	Leu	Arg	
245			420						425					430			
247	atg	gta	gca	gcc	att	gcc	gta	ctg	aca	aag	gat	gca	ggc	aag	cta	acc	1344
248	Met	Val	Ala	Ala	Ile	Ala	Val	Leu	Thr	Lys	Asp	Ala	Gly	Lys	Leu	Thr	
249			435				440							445			
251	atg	gga	cag	cca	cta	gtc	att	ctg	gcc	ccc	cat	gca	gta	gag	gca	cta	1392
252	Met	Gly	Gln	Pro	Leu	Val	Ile	Leu	Ala	Pro	His	Ala	Val	Glu	Ala	Leu	

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253      450      455      460
255 gtc aaa caa ccc ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac      1440
256 Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His
257 465      470      475      480
259 tat cag gcc ttg ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg      1488
260 Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val
261      485      490      495
263 gta gcc ctg aac ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg      1536
264 Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu
265      500      505      510
267 caa cac aac tgc ctt gat aat tcc cgc tta att aat taa      1575
268 Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn
269      515      520
272 <210> SEQ ID NO: 6
274 <211> LENGTH: 524
276 <212> TYPE: PRT
278 <213> ORGANISM: Moloney-Murine Leukemia Virus
281 <400> SEQUENCE: 6
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284 1      5      10      15
287 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
288      20      25      30
291 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
292      35      40      45
295 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
296      50      55      60
299 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
300 65      70      75      80
303 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
304      85      90      95
307 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
308      100      105      110
311 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
312      115      120      125
315 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu
316      130      135      140
319 Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu
320 145      150      155      160
323 Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe
324      165      170      175
327 Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu
328      180      185      190
331 Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg
332      195      200      205
335 Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu
336      210      215      220
339 His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu
340 225      230      235      240
343 Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp

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344          245          250          255
347 Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly
348          260          265          270
351 Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys
352          275          280          285
355 Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala
356          290          295          300
359 Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln
360 305          310          315          320
363 Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro
364          325          330          335
367 Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly
368          340          345          350
371 Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile
372          355          360          365
375 Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr
376          370          375          380
379 Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly
380 385          390          395          400
383 Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu
384          405          410          415
387 Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg
388          420          425          430
391 Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr
392          435          440          445
395 Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu
396          450          455          460
399 Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His
400 465          470          475          480
403 Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val
404          485          490          495
407 Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu
408          500          505          510
411 Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn
412          515          520

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VERIFICATION SUMMARY

DATE: 12/20/2004

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